

ABSTRACT

Methods and apparatuses for sequencing single polymer molecules, such as a nucleic acid strand, are discussed. A discussed method comprises dividing a polymer sample into a number of polymer subsamples equal to the number of different monomer types and partially labeling only one of the monomer types in each polymer subsample. The method may further comprise placing a subsample into a reaction chamber, sequentially separating each monomer from the polymer subsample, and detecting the labels of each separated labeled monomer as a function of time. The time between each labeled monomer may be used to construct a monomer-time map for each polymer sub-sample using overlapping data analysis and frequency analysis. Time maps may then be assembled/aligned into a polymer sequence from the monomer-time maps of each of the polymer subsamples using non-overlapping data analysis.